



-1-

SEQUENCE LISTING

<110> Gray et al.

<120> MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC INHIBITOR SUBSTANCES, AND USES THEREOF

<130> 27866/34810

<140> 09/509,165

<141> 2000-06-12

<150> 09/067,447

<151> 1998-04-28

<150> 08/939,107

<151> 1997-09-26

<150> 08/660,542

<151> 1996-06-07

<150> 08/558,658

<151> 1995-11-16

<150> 08/479,620

<151> 1995-06-07

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 2923

<212> DNA

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<222> (20)..(298)

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<221> mat_peptide

<222> (92)..(298)

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-20

-15

ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100

Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr

-10

-5

-1 1

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ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148
 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
 5 10 15
 cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196
 Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
 20 25 30 35
 tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc 244
 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
 40 45 50
 tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292
 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
 55 60 65
 agc caa tgaagagcct actctgatga ccgtggcctt ggctcctcca ggaaggctca 348
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<210> 2
<211> 93
<212> PRT
<213> Homo sapiens - human MDC

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 -20 -15 -10
Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
 -5 -1 1 5
Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 10 15 20
Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
 25 30 35 40
Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
 45 50 55
Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

<210> 3
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer JHSP6

<400> 3
gacactatag aatagggc

18

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer M13

<400> 4
gtaaaacgac-ggccagt

17

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer T3.1

<400> 5

aattaaccct cactaaaggg

20

<210> 6

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer T7.1

<400> 6

gtaatacgac tcactatagg gc

22

<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-1F

<400> 7

tctatctaga ggcccctacg gcgccaacat ggaag

35

<210> 8

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-2R

<400> 8

caccggatcc tcattggctc agcttattga gaa

33

<210> 9

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-4R

<400> 9

aatggatcca cagcacggag gtgaccaag

29

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-3R

<400> 10
agtcaagctt agggcactct gggatcggca c

31

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-FX2

<400> 11
tatcggatcc tggttccgcg tggcccctac ggcgccaaca tggaa

45

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer GEX5

<400> 12
gaaatccagc aagtatatag ca

22

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-Pel

<400> 13
attgccatgg ccggccccta cggcgccaac atggaa

36

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcH

<400> 14

gaccaagctt gagacatata ggacagagca

30

<210> 15

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcX

<400> 15

tggatctaga agttggcaca ggcttctgg

29

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer DC03

<400> 16

cgaaattaat acgactcact

20

<210> 17

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
390mycRX

<400> 17

tggatctaga tcaattcaag tectctcgc tgatcagctt ctgctcttgg ctcagcttat 60

tgagaat

67

<210> 18

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-3

<220>

<400> 18

Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala
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Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr
-5 1 5

Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu
10 15 20 25

Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
30 35 40

Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
45 50 55

Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
60 65 70

Pro Lys Leu
75

<210> 19

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-1

<400> 19

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
-20 -15 -10

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
-5 1 5

Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
10 15 20 25

Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
30 35 40

Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
45 50 55

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
60 65 70

Pro Lys Thr
75

<210> 20

<211> 76

<212> PRT

<213> Homo sapiens - Hu MCP-2

<220>

<400> 20

Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
1 5 10 15

Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly
35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
50 55 60

Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
65 70 75

<210> 21

<211> 91

<212> PRT

<213> Homo sapiens - RANTES

<220>

<400> 21

Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala
-20 -15 -10

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
-5 1 5

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
10 15 20 25

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
30 35 40

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
45 50 55

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
60 65

<210> 22

<211> 91

<212> PRT

<213> Homo sapiens - MIP-1 beta

<220>

<400> 22

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
-20 -15 -10

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
-15 1 5

Ala Cys Cys Phe Ser Tyr Thr Arg Glu Ala Ser Ser Asn Phe Val Val
10 15 20

Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe
30 35 40

Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp
45 50 55

Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
60 65

<210> 23

<211> 92

<212> PRT

<213> Homo sapiens - MIP-1 alpha

<220>

<400> 23

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
-20 -15 -10

Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
-5 1 5 10

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
15 20 25

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
30 35 40

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
45 50 55

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
60 65 70

<210> 24

<211> 96

<212> PRT

<213> Homo sapiens - I-309

<220>

<400> 24

Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
-20 -15 -10

Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg

-5		1		5											
Cys	Cys	Phe	Ser	Phe	Ala	Glu	Gln	Glu	Ile	Pro	Leu	Arg	Ala	Ile	Leu
10				15					20					25	
Cys	Tyr	Arg	Asn	Thr	Ser	Ser	Ile	Cys	Ser	Asn	Glu	Gly	Leu	Ile	Phe
			30					35					40		
Lys	Leu	Lys	Arg	Gly	Lys	Glu	Ala	Cys	Ala	Leu	Asp	Thr	Val	Gly	Trp
		45				50						55			
Val	Gln	Arg	His	Arg	Lys	Met	Leu	Arg	His	Cys	Pro	Ser	Lys	Arg	Lys
	60					65						70			

<210> 25
 <211> 93
 <212> PRT
 <213> Artificial Sequence - Human MDC analog

<220>
 <223> The amino acid at position 24 is selected from the group consisting of arg, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp, aspartate, glutamate, asn, gln, cys, and met

<220>
 <223> The amino acid at position 27 is independently selected from the group consisting of lys, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp, aspartate, glutamate, asn, gln, cys, and met

<220>
 <223> The amino acid at position 30 is independently selected from the group consisting of tyr, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<220>
 <223> The amino acid at position 50 is independently selected from the group consisting of glu, lys, arg, his, gly, and ala

<220>
 <223> The amino acid at position 59 is independently selected from the group consisting of trp, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<220>

<223> The amino acid at position 60 is independently selected from the group consisting of val, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<400> 25

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Xaa
10 15 20

Val Val Xaa His Phe Xaa Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Xaa Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Xaa Xaa Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 26

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-7F

<400> 26

tattggatcc gttctagctc cctgttctcc

30

<210> 27

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-8R

<400> 27

ccaagaattc ctgcagccac tttctgggct c

31

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA1

<400> 28

gcgactctct actgtttctc

20

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA2

<400> 29

cacaggaaac agctatgacc

20

<210> 30

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 30

Leu Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp
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Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp
20 25 30

Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg
35 40 45

Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile
50 55 60

Leu Asn Lys Leu Ser Gln
65 70

<210> 31

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 31

Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Tyr Leu Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 32

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 32

Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys Glu Tyr Phe Tyr Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 33

<211> 1677

<212> DNA

<213> Homo sapiens - human CCR4 cDNA

<220>

<221> CDS

<222> (183)..(1262)

<400> 33

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agaaaagcaa gctgcttctg gttgggacca gacctgcctt gaggagcctg tagagttaaa 180

aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile

1 5 10 15

tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275

Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys

20 25 30

gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323

Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser

35 40 45

ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371

Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val

50 55 60

ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419

Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu

65 70 75

aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467

Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp

80 85 90 95

ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag 515

Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys

100 105 110

atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt 563

Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe

115 120 125

gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg 611

Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val

130 135 140

ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg 659

Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu

145 150 155

gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc 707

Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe

160 165 170 175

agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac 755

Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr

180 185 190

tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac 803
 Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn
 195 200 205

att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc 851
 Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser
 210 215 220

atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag 899
 Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys
 225 230 235

gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg 947
 Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp
 240 245 250 255

aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa 995
 Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu
 260 265 270

gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag 1043
 Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln
 275 280 285

gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc 1091
 Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile
 290 295 300

tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc 1139
 Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe
 305 310 315

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc 1187
 Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu
 320 325 330 335

caa att tac tct gct gac acc ccc agc tca tct tac acc cag tcc acc 1235
 Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr
 340 345 350

atg gat cat gat ctt cat gat gct ctg taggaaaaat gaaatggtga 1282
 Met Asp His Asp Leu His Asp Ala Leu
 355 360

aatgcagagt caatgaactt ttccacattc agagcttact ttaaaattgg tatttttagg 1342

taagagatcc ctgagccagt gtcaggagga aggcttacac ccacagtgga aagacagctt 1402

ctcctctgc aggcagcttt ttctctccca ctagacaagt ccagcctggc aagggttcac 1462

ctgggctgag gcctccttcc tcacaccagg cttgcttgca ggcattgagtc agtctgatga 1522

gaactctgag cagtgttga atgaagttgt aggtaatatt gcaaggcaaa gactattccc 1582

ttctaacctg aactgatggg tttctccaga gggaattgca gagtactggc tgatggagta 1642:
aatcgctacc ttttgctgtg gcaaattgggc ccccg 1677

<210> 34

<211> 360

<212> PRT

<213> Homo sapiens - human CCR4

<400> 34

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15
Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30
Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45
Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60
Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80
Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95
Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110
Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125
Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140
Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160
Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165 170 175
Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
180 185 190
Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
195 200 205
Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
340 345 350

Asp His Asp Leu His Asp Ala Leu
355 360

<210> 35
<211> 1784
<212> DNA
<213> murine MDC cDNA

<220>
<221> CDS
<222> (1)..(276)

<220>
<221> mat_peptide
<222> (73)..(276)

<400> 35
atg tct aat ctg cgt gtc cca ctc ctg gtg gct ctc gtc ctt ctt gct 48
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala
-20 -15 -10

gtg gca att cag acc tct gat gca ggt ccc tat ggt gcc aat gtg gaa 96
Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
-5 -1 1 5

gac agt atc tgc tgc cag gac tac atc cgt cac cct ctg cca tca cgt 144
 Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
 10 15 20

tta gtg aag gag ttc ttc tgg acc tca aaa tcc tgc cgc aag cct ggc 192
 Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
 25 30 35 40

gtt gtt ttg ata acc gtc aag aac cga gat atc tgt gcc gat ccc agg 240
 Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
 45 50 55

cag gtc tgg gtg aag aag cta ctc cat aaa ctg tcc tagggaggag 286
 Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
 60 65

gacctgatga ccatgggtet ggtgtggtcc agggaggctc agcaagccct attcttctgc 346
 cattccagca agagccttgc caacgaagcc acctttactc acctccatcc cctgggctgt 406
 cactctgtca ggctctggtc cctctacctc cctctatcc ctccagctt atcccccttc 466
 aatgtggcag ctgggaaaca cattcaggcc agccttacc aatgctact cccactgct 526
 ttagatgaga ccagcgtcct tgttttgatg ccttgatcct atgatgcctt cccatcccc 586
 agccttggcc ccttctctt cttgcatgta gggaaggccc ataggtttca aatatgtgct 646
 acctacttcc ctttctgggg ggttctaata ccagcatgt ttttctgct gcaggcacct 706
 atccagtgcc acacacctcc caagtttcta tcagtccag tgggcatcca ccaagcccca 766
 aacttcagac ttcttggcc tccacctact ctcatagaa ttctgggagt ttcaggctgg 826
 tccaccaggc ccccagggt taggccaagg ccccaccag agctctcct gtttcttgg 886
 ctgcagcagc gggcagggag caaggagcag gctcagaatc agatttctta aaggagctgc 946
 agactccatc agtaaaagga atctttctcc catcctgaa tataaggcag ttttctgtca 1006
 acacagagac tcaggttggt agaaatggcc acatagatca actgtgaaac cctaaattta 1066
 ccaagaatca acttccaccc ctcttcaacc acatgctagg gtcttttact ttctctgccc 1126
 cacacctttg actccttgcc tgtgtagctg atagtgaag ttatgctatg gtgtcagtga 1186
 ctgccacagt ttgtttggta ttataagcta tagttatatt tatataggaa agaggataaa 1246
 tatatgtggg ccaaatagac gaactggaga gttttaggat ctgggggcag gaagggccat 1306
 acaaagtgat acctcagaaa atagatgggt gtgggagctg ctgccagtgg cagagttaac 1366
 ttaaagaact taattgaaat tattcttgag tggctgagcc caagacaaga atatagaacc 1426

cattcttgct tccctggaga caacagtggc cccaggggaa ggaataaacc ttcttgctcc 1486
tctggaggga gcatggcctg rcttagccga gtgactggac tgtgtgagat tggggggcatc 1546
gcttttctcty tctgagcctc agctgacagc atatggggacc aaaaaggget tgatccaaac 1606
cacaggggatt gacagtgccca gccacagctg tgtccagggc tegtgttctg ccagaaggag 1666
caactggacg accagggcca ccaactagtgc tactttgctc actgcccacg catgtcctga 1726
aggccctccc cctctctctc ctacttctgg gaaaataaat gctcgccaat aatacctg 1784

<210> 36
<211> 92
<212> PRT
<213> murine MDC

<400> 36
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala
 -20 -15 -10

Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
 -5 -1 1 5

Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
 10 15 20

Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
 25 30 35 40

Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
 45 50 55

Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
 60 65

<210> 37
<211> 958
<212> DNA
<213> rat MDC cDNA

<220>
<221> CDS
<222> (1)..(243)

<220>
<221> mat_peptide
<222> (40)..(243)

<400> 37

ctc gtc ctt ctt gct gtg gca ctt cag acc tcc gat gca ggt ccc tat 48
Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
-10 -5 -1 1

ggt gcc aat gtg gaa gac agt atc tgc tgc cag gac tac atc cgt cac 96
Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
5 10 15

cct ctg cca cca cgt ttc gtg aag gag ttc tac tgg acc tca aag tcc 144
Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35

tgc cgc aag cct ggc gtc gtt ttg ata acc atc aag aac cga gat atc 192
Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
40 45 50

tgt gct gac ccc ang atg ctc tgg gtg aag aag ata ctc cac aag ttg 240
Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
55 60 65

gcc tagggagaag ggctgatga ccacgggtct ggtgtctcca caaggctcag 293
Ala

caaaccctat ccttctgcca tccagcaaga gccttgccaa caactccacc ttgtctcacc 353

tccatccctt gggttgtcac tctgtgaagc ctgggtccc tgtacttct gtccgtcccc 413

tccagctcat tctcttccaa cgtggcagcc gggaagcaact tctggctagc cttacccaat 473

actactcccc actgetttaa atgagaccag ggtccttgtt ttgtgcctt tggatcctat 533

gatgccttcc cagtctccag ccttggcccc ctctcttct tacatgtagg gaacaccaat 593

atctttcaag tatgtgtac ccaattctc tctctggag gctgctgga cccggaatat 653

tatccctgc tgcaggect tccaagcacc actcactcc caggcttcc atcgtccca 713

gtcccaagcc ccatgcttca gaacttcc tggcccccc ctacactcca caaattctgg 773

ggaagtctca cnaactgggt cccctcagc cccacggga aggaaggtcc ccnccaaca 833

acntctctt gttttcccc gtctccncc nccgggant gggnccna atccccatt 893

tctgaanang aacngccat tctcccntt aaaattaacc tttcccccc tccctgangt 953

taggn 958

<210> 38

<211> 81

<212> PRT

<213> rat

<400> 38
 Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
 -10 -5 -1 1
 Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
 5 10 15
 Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
 20 25 30 35
 Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
 40 45 50
 Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
 55 60 65

Ala

<210> 39
 <211> 506
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: S. cerevisiae alpha factor pre-
 pro/human MDC cDNA chimeric construct
 <221> CDS
 <222> (15) .. (476)

<220>
 <221> mat_peptide
 <222> (270) .. (476)
 <400> 39

atctcgagct cacg atg aga ttt cdt tca att ttt act gea gtt tta ttc 50
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe
 -85 -80 -75
 gca gca tcc tcc gca tta gct gct cca gtc aac act aca aca gaa gat 98
 Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp
 -70 -65 -60
 gaa acg gca caa att ccg gct gaa gct gtc atc ggt tac tta gat tta 146
 Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu
 -55 -50 -45
 gaa ggg gat ttc gat gtt gct gtt ttg cca ttt tcc aac agc aca aat 194
 Glu Gly Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn
 -40 -35 -30

aac ggg tta ttg ttt ata aat act act att gcc agc att gct gct aaa 242
 Asn Gly Leu Leu Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys
 -25 -20 -15 -10

gaa gaa ggg gta cct ttg gat aaa aga ggc ccc tac ggc gcc aac atg 290
 Glu Glu Gly Val Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met
 -5 -1 1 5

gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg 338
 Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu
 10 15 20

cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccg agg cct 386
 Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro
 25 30 35

ggc gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc 434
 Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro
 40 45 50 55

aga gtg ccc tgg gtg aag atg att ctc aat aag ctg agc caa 476
 Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

tgaaggcctt ctagagcggc cgcacgata 506

<210> 40
 <211> 154
 <212> PRT
 <213> cDNA
 <400> 40

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75 -70

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 -65 -60 -55

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
 -50 -45 -40

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -35 -30 -25

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -20 -15 -10

Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val
 -5 -1 1 5 10

Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys
 15 20 25

His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu
30 35 40

Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp
45 50 55

Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 41
<211> 93
<212> PRT
<213> Artificial Human MDC analog

<220>
<223> The amino acid at position 2 is not proline
<220>

<400> 41
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Xaa Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 42
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (53)..(334)

<220>
<221> mat_peptide
<222> (122)..(334)

<400> 42

ccctgagcag agggacctgc acacagagac tccctcctgg gctcctggca cc atg gcc 58
Met Ala

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
-20 -15 -10

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
-5 -1 1 5 10

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
15 20 25

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
30 35 40

gtg cag ggc agg gcc atc tgt tgc gac ccc aac aac aag aga gtg aag 298
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
45 50 55

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tgaagcctcc 344
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
60 65 70

tcaccccgaga ctctgactg tctcccgga ctacctggga cctccaccgt tgggtgttcac 404

cgccccacc ctgagcgct ggggtccaggg gaggccttcc agggacgaag aagagccaca 464

gtgagggaga tcccatcccc ttgtctgaac tggagccatg ggcacaaagg gccagatta 524

aagtctttat cctc 538

<210> 43
<211> 94
<212> PRT
<213> Homo sapiens

<400> 43
Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala
-20 -15 -10

Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
-5 -1 1 5

Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
10 15 20 25

Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
30 35 40

Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
45 50 55

Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
60 65 70

<210> 44
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
atgggacat atggagcaaa tatggaagat agt

33

<210> 45
<211> 335
<212> DNA
<213> Macaque MDC

<220>
<221> CDS
<222> (19)..(297)

<400> 45
agacatacag gacagagc atg gct cgc cta cag act gtg ttc ctg ggt gtc
Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val

51

-20

-15

ctc atc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tat
Leu Ile Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
-10 -5 -1 1

99

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
5 10 15

147

cgt atg ccc ctg cgt gtg gtg aaa cac ttc tac tgg acc tca gac tcc
Arg Met Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
20 25 30 35

195

tgc ccg agg cct ggc gtg gtg ttg cta acc tcc agg gat aag gag atc
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile
40 45 50

243

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
55 60 65

291

agc caa tgaagagcct actatgatga ccgtggccta agcaagcc
Ser Gln

335

<210> 46
<211> 93
<212> PRT
<213> Macaque MDC

<400> 46
Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val Leu Ile Leu Leu Ala
1 5 10 15

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
20 25 30

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Met Pro Leu Arg
35 40 45

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
50 55 60

Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
65 70 75 80

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
85 90

1
Candid